

SEARCH REQUEST FORM

Requestor's
Name: _____

Serial
Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 12-12-02

Searcher: Beverly 24994

Terminal time: 28

Elapsed time: _____

CPU time: _____

Total time: 33

Number of Searches: _____

Number of Databases: 1

Search Site

_____ STIC

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Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

☒ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

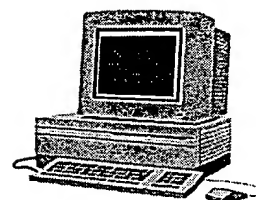
☒ Other CGN

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Search Results

Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, **CM1-1E01** or e-mail **mary.hale@uspto.gov**.

09/750609

L1 FILE 'REGISTRY' ENTERED AT 10:14:02 ON 12 DEC 2002
123 S CCTTCTC[CG]CCCTGTT/SQSN

L2 FILE 'HCAPLUS' ENTERED AT 10:18:27 ON 12 DEC 2002
27 S L1

L2 ANSWER 1 OF 27 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:696159 HCAPLUS
DOCUMENT NUMBER: 137:246071
TITLE: Gene expression profiles relating to normal and
osteoarthritic cartilage
INVENTOR(S): Liew, Choong-Chin; Marshall, Wayne E.; Zhang,
Hongwei
PATENT ASSIGNEE(S): Chondrogene Inc., Can.
SOURCE: PCT Int. Appl., 777 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002070737	A2	20020912	WO 2002-CA247	20020228
WO 2002070737	C1	20021031		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:
US 2001-271955P P 20010228
US 2001-275017P P 20010312
US 2001-305340P P 20010713

AB The invention provides gene expression profiles comprising one or more polynucleotide sequences that are expressed in chondrocytes from any of the following developmental and disease stages: fetus, normal adult, mild osteoarthritis, moderate osteoarthritis, marked osteoarthritis, and severe osteoarthritis. Complementary DNA libraries were constructed from human fetal, normal, mild osteoarthritic and severe osteoarthritic cartilage samples (13,398, 17,151, 12,651, and 14,222 expressed sequence tags (ESTs), resp.). The known and novel clones derived from these libraries were then used to construct human chondrocyte-specific microarrays to generate differential gene expression profiles useful as a diagnostic tools for detection of osteoarthritis. A total of 5807 expressed gene sequences are provided and matched to known gene sequences, other ESTs, or mitochondrial, ribosomal, vector, and cDNA/hypothetical protein sequences in the public databases. Arrays of the invention are useful as a gold std. for osteoarthritis diagnosis and for use to identify and monitor therapeutic efficacy of new drug targets.

IT 285540-13-8
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

09/750609

(Biological study)
(nucleotide sequence; gene expression profiles relating to normal
and osteoarthritic cartilage)

L2 ANSWER 2 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2002:125915 HCAPLUS

DOCUMENT NUMBER: 137:58620

TITLE: Nucleic acids differentially expressed in human
prostate cancer and methods for identification,
assessment, prevention, and therapy of prostate
cancer

INVENTOR(S): Schlegel, Robert; Endege, Wilson O.; Monahan,
John E.

PATENT ASSIGNEE(S): Millennium Predictive Medicine, Inc., USA

SOURCE: PCT Int. Appl., 11750 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 14

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001060860	A2	20010823	WO 2001-XK5171	20010220
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
WO 2001060860	A2	20010823	WO 2001-US5171	20010220
WO 2001060860	A3	20020613		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.:
US 2000-183319P P 20000217
US 2000-189862P P 20000316
US 2000-207454P P 20000525
US 2000-211314P P 20000609
US 2000-219007P P 20000718
US 2000-255281P P 20001213
WO 2001-US5171 W 20010220

AB The invention relates to compns., kits, and methods for detecting, characterizing, preventing, and treating human prostate cancers. At least 22,548 of previously unidentified cDNA markers are provided, wherein changes in the levels of expression of one or more of the

markers is correlated with the presence of prostate cancer. These nucleotide sequences were identified through subtracted library expts. using a PCR-based method that allows the isolation of clones expressed at higher levels in one population of mRNA (tester) compared to another population (driver). Both tester and driver mRNA populations are converted into cDNA by reverse transcription, PCR amplified, and then hybridized using the PCR-Select cDNA subtraction kit from Clontech. After generation of the subtractive libraries, a group of 96 or more clones from each library is tested to confirm differential expression by reverse Southern hybridization. Methods are provided for detecting the presence of prostate cancer in a sample, the absence of prostate cancer in a sample, the stage of a prostate cancer, the metastatic potential of prostate cancer, the indolence or aggressiveness of the cancer, and other characteristics of prostate cancer that are relevant to prevention, diagnosis, characterization, and therapy of prostate cancer in a patient. [This abstr. record is one of fifteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 438805-25-5

RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; nucleic acids differentially expressed in human prostate cancer and methods for identification, assessment, prevention, and therapy of prostate cancer)

L2 ANSWER 3 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2002:96620 HCAPLUS

DOCUMENT NUMBER: 136:129773

TITLE: Construction and analysis of a human-chimpanzee comparative clone map

AUTHOR(S): Fujiyama, Asao; Watanabe, Hidemi; Toyoda, Atsushi; Taylor, Todd D.; Itoh, Takehiko; Tsai, Shih-Feng; Park, Hong-Seog; Yaspo, Marie-Laure; Lehrach, Hans; Chen, Zhu; Fu, Gang; Saitou, Naruya; Osoegawa, Kazutoyo; de Jong, Pieter J.; Suto, Yumiko; Hattori, Masahira; Sakaki, Yoshiyuki

CORPORATE SOURCE: RIKEN Genomic Sciences Center, Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
SOURCE: Science (Washington, DC, United States) (2002), 295(5552), 131-134

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The recently released human genome sequences provides ref. data to conduct comparative genomic research on primates, which will be important to understand what genetic information makes us human. Here, a first-generation human-chimpanzee comparative genome map and its initial anal. is presented. The map was constructed through paired alignment of 77,461 chimpanzee bacterial artificial chromosome end sequences with publicly available human genome sequences. Candidate positions were detected, including two clusters on human chromosome 21 that suggest large, nonrandom

regions of difference between the two genomes. The sequence data is available in GenBank under Accession Nos. AG029037-AG186569 and AG186783-AG187837. [This abstr. record is one of forty records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **368618-05-7**, GenBank AG100084

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; construction and anal. of a human-chimpanzee comparative clone map)

L2 ANSWER 4 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2002:44982 HCAPLUS

DOCUMENT NUMBER: 137:1254

TITLE: Generation and comparative analysis of .apprx.3.3 Mb of mouse genomic sequence orthologous to the region of human chromosome 7q11.23 implicated in williams syndrome

AUTHOR(S): DeSilva, Udaya; Elnitski, Laura; Idol, Jacquelyn R.; Doyle, Johannah L.; Gan, Weiniu; Thomas, James W.; Schwartz, Scott; Dietrich, Nicole L.; Beckstrom-Sternberg, Stephen M.; McDowell, Jennifer C.; Blakesley, Robert W.; Bouffard, Gerard G.; Thomas, Pamela J.; Touchman, Jeffrey W.; Miller, Webb; Green, Eric D.

CORPORATE SOURCE: Genome Technology Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, 20892, USA

SOURCE: Genome Research (2002), 12(1), 3-15

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Williams syndrome is a complex developmental disorder that results from the heterozygous deletion of a .apprx.1.6-Mb segment of human chromosome 7q11.23. These deletions are mediated by large (.apprx.300 kb) duplicated blocks of DNA of near-identical sequence. Previously, we showed that the orthologous region of the mouse genome is devoid of such duplicated segments. Here, we extend our studies to include the generation of .apprx.3.3 Mb of genomic sequence from the mouse Williams syndrome region, of which just over 1.4 Mb is finished to high accuracy. Comparative analyses of the mouse and human sequences within and immediately flanking the interval commonly deleted in Williams syndrome have facilitated the identification of nine previously unreported genes, provided detailed sequence-based information regarding 30 genes residing in the region, and revealed a no. of potentially interesting conserved noncoding sequences. Finally, to facilitate comparative sequence anal., we implemented several enhancements to the program PipMaker, including the addn. of links from annotated features within a generated percent-identity plot to specific records in public databases. Taken together, the results reported here provide an important comparative sequence resource that should catalyze addnl. studies of Williams syndrome, including those that aim to characterize genes within the commonly deleted interval and to develop mouse models of the disorder.

IT **312980-59-9**, GenBank AC087420

09/750609

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(nucleotide sequence; generation and comparative anal. of mouse
genomic sequence orthologous to the region of human chromosome
7q11.23 implicated in Williams syndrome)

REFERENCE COUNT: 120 THERE ARE 120 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 5 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:868629 HCAPLUS

DOCUMENT NUMBER: 136:15957

TITLE: Human nucleic acids and their encoded proteins
and antibodies

INVENTOR(S): Birse, Charles E.; Rosen, Craig A.

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA

SOURCE: PCT Int. Appl., 2081 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 90

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001090304	A2	20011129	WO 2001-US16450	20010518
WO 2001090304	A3	20020510		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
AU 2001074888	A5	20011203	AU 2001-74888	20010518
PRIORITY APPLN. INFO.:			US 2000-205515P P	20000519
			WO 2001-US16450 W	20010518

AB The present invention relates to 1405 novel human polynucleotides and the polypeptides encoded by these polynucleotides and the use of the polypeptides for detecting disorders. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the prodn. and function of the polypeptides of the present invention.

IT 376407-32-8P

RL: ANT (Analyte); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST

09/750609

(Analytical study); BIOL (Biological study); PREP (Preparation);
USES (Uses)
(nucleotide sequence; human nucleic acids and their encoded
proteins and antibodies)

L2 ANSWER 6 OF 27 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:831767 HCAPLUS
DOCUMENT NUMBER: 137:88421
TITLE: Genetic polymorphisms in genes associated with
drug metabolism and their use in selecting drug
therapies
INVENTOR(S): Stanton, Vincent; Zillmann, Martin
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 210 pp., Cont.-in-part of
U.S. Ser. No. 710,467.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2001034023	A1	20011025	US 2000-733000	20001207
WO 2000050639	A2	20000831	WO 2000-US1392	20000120
WO 2000050639	A3	20020510		

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN,
IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD,
MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ,
BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 2001034023 A1 20011025 US 2000-733000 20001207
PRIORITY APPLN. INFO.: US 1999-131334P P 19990426
US 1999-139440P P 19990615
WO 2000-US1392 W 20000120
US 2000-696482 A2 20001024
US 2000-710467 A2 20001108
US 2000-733000 A 20001207
US 1999-121047P P 19990222
US 1999-357743 A 19990720

AB Methods for identifying and utilizing variances in genes relating to
efficacy and safety of medical therapy and other aspects of medical
therapy are described, including methods for selecting an effective
treatment. [This abstr. record is one of several records for this
document necessitated by the large no. of index entries required to
fully index the document and publication system constraints.].

IT 391524-07-5, GenBank M65105

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(nucleotide sequence; genetic polymorphisms in genes assocd. with
drug metab. and their use in selecting drug therapies)

L2 ANSWER 7 OF 27 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:829016 HCAPLUS

Searcher : Shears 308-4994

09/750609

DOCUMENT NUMBER: 136:49172
TITLE: Mouse BAC ends quality assessment and sequence analyses
AUTHOR(S): Zhao, Shaying; Shatsman, Sofiya; Ayodeji, Bola; Geer, Keita; Tsegaye, Getahun; Krol, Margaret; Gebregeorgis, Elizabeth; Shvartsbeyn, Alla; Russell, Daniel; Overton, Larry; Jiang, Lingxia; Dimitrov, George; Tran, Kevin; Shetty, Jyoti; Malek, Joel A.; Feldblyum, Tamara; Nierman, William C.; Fraser, Claire M.
CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA
SOURCE: Genome Research (2001), 11(10), 1736-1745
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A large-scale BAC end-sequencing project at The Institute for Genomic Research (TIGR) has generated one of the most extensive sets of sequence markers for the mouse genome to date. With a sequencing success rate of >80%, an av. read length of 485 bp, and ABI3700 capillary sequencers, 449,234 nonredundant mouse BAC end sequences (mBESs) have been generated with 218 Mb total from 257,318 clones from libraries RPCI-23 and RPCI-24, representing 15.times. clone coverage, 7% sequence coverage, and a marker every 7 kb across the genome. A total of 191,916 BACs have sequences from both ends providing 12.times. genome coverage. The av. Q20 length is 406 bp and 84% of the bases have phred quality scores .gtoreq. 20. RPCI-24 mBESs have more Q20 bases and longer reads on av. than RPCI-23 sequences. ABI3700 sequencers and the sample tracking system ensure that >95% of mBESs are assocd. with the right clone identifiers. A significant fraction of mBESs contains LI repeats and .apprx.48% of the clones have both ends with .gtoreq.100 bp contiguous unique Q20 bases. About 3% mBESs match ESTs and >70% of matches were conserved between the mouse and the human or the rat. Approx. 0.1% mBESs contain STSs. About 0.2% mBESs match human finished sequences and >70% of these sequences have EST hits. The analyses indicate that our high-quality mouse BAC end sequences will be a valuable resource to the community. [This abstr. record is one of 100 records necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT 283872-10-6, GenBank AZ284882
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; mouse BAC ends quality assessment and sequence analyses)

L2 ANSWER 8 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:747969 HCAPLUS
DOCUMENT NUMBER: 135:299570
TITLE: Human nucleic acids and polypeptides and their diagnostic and therapeutic uses
INVENTOR(S): Drmanac, Rodoje T.; Liu, Chenghua; Tang, Y. Tom
PATENT ASSIGNEE(S): Hyseq, Inc., USA
SOURCE: PCT Int. Appl., 103 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English

Searcher : Shears 308-4994

09/750609

FAMILY ACC. NUM. COUNT: 76

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001075067	A2	20011011	WO 2001-US8631	20010330
WO 2001075067	A3	20020404		
WO 2001075067	C2	20021031		
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WO 2001075067	A2	20011011	WO 2001-XA8631	20010330
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WO 2001075067	A2	20011011	WO 2001-XB8631	20010330
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WO 2001075067	A2	20011011	WO 2001-XC8631	20010330
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Searcher : Shears 308-4994

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WO 2001075067 A2 20011011 WO 2001-XE8631 20010330
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WO 2001075067 A2 20011011 WO 2001-XF8631 20010330
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WO 2001075067 A2 20011011 WO 2001-XG8631 20010330
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RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
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WO 2001075067 A2 20011011 WO 2001-XH8631 20010330
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GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
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WO 2001075067 A2 20011011 WO 2001-XI8631 20010330

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W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
TG

AU 2001049251	A5	20011015	AU 2001-49251	20010330
PRIORITY APPLN. INFO.:			US 2000-540217	A 20000331
			US 2000-649167	A 20000823
			WO 2001-US8631	W 20010330

AB The present invention provides 30,368 nucleic acids and the 30,368 novel human polypeptide sequences encoded by these nucleic acids. A plurality of novel nucleic acids are obtained from cDNA libraries prep'd. from various human tissues and in some cases isolated from a genomic library derived from human chromosomes using std. PCR, sequencing by hybridization signature anal., and Sanger sequencing techniques. Nearest neighbor results are identified by sequence homol. searching. The invention also relates to therapeutic, diagnostic, and research utilities for these polynucleotides and proteins. [This abstr. record is the first of ten records for this document necessitated by the large no. of index entries required to fully index the document and publication ssystem constraints.].

IT 365592-77-4

RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(nucleotide sequence; human nucleic acids and polypeptides and their diagnostic and therapeutic uses)

L2 ANSWER 9 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:618209 HCAPLUS

DOCUMENT NUMBER: 135:193985

TITLE: Genes expressed in tumor cells and their use as diagnostic markers and the assessment of tumors to chemotherapy

INVENTOR(S): Roth, Frederick P.; Van Huffel, Christophe;
White, James V.; Shyjan, Andrew W.

PATENT ASSIGNEE(S): Millennium Predictive Medicine, Inc., USA

SOURCE: PCT Int. Appl., 122 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001061050	A2	20010823	WO 2001-US5301	20010216

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,

Searcher : Shears 308-4994

09/750609

PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ,
TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
TG

US 2002120004 A1 20020829 US 2001-788099 20010216
PRIORITY APPLN. INFO.: US 2000-183265P P 20000217

AB The present invention is directed to the identification of markers that can be used to det. the sensitivity of cancer cells to a therapeutic agent. The present invention is also directed to the identification of therapeutic targets. Nucleic acid arrays were used to det. the level of expression of sequences (genes) found in 60 different solid tumor cancer cell lines selected from the NCI 60 cancer cell line series. Expression anal. was used to identify markers assocd. with sensitivity to certain chemotherapeutic agents.

IT 136252-70-5, GenBank M65105

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; genes expressed in tumor cells and their use as diagnostic markers and assessment of tumors to chemotherapy)

L2 ANSWER 10 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:618207 HCAPLUS

DOCUMENT NUMBER: 135:190398

TITLE: Nucleic acid markers useful for the identification, assessment, prevention and therapy of human cancers

INVENTOR(S): Roth, Frederick P.; Van Huffel, Christophe; White, James V.; Shyjan, Andrew W.

PATENT ASSIGNEE(S): Millennium Predictive Medicine, Inc., USA

SOURCE: PCT Int. Appl., 126 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001061048	A2	20010823	WO 2001-US5263	20010216
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

US 2002051978 A1 20020502 US 2001-788100 20010216
PRIORITY APPLN. INFO.: US 2000-183312P P 20000217

AB The present invention is directed to the identification of markers that can be used to det. the sensitivity of cancer cells to a

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therapeutic agent. The present invention is also directed to the identification of therapeutic targets. Nucleic acid arrays were used to det. the level of expression of sequences (genes) found in 60 different solid tumor cancer cell lines selected from the NCI 60 cancer cell line series. Expression anal. was used to identify markers assocd. with sensitivity to certain chemotherapeutic agents.

IT 136252-70-5, GenBank M65105

RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(nucleotide sequence; nucleic acid markers useful for the identification, assessment, prevention and therapy of human cancers)

L2 ANSWER 11 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:565201 HCAPLUS

DOCUMENT NUMBER: 135:163399

TITLE: Human nucleic acids and their encoded proteins and antibodies

INVENTOR(S): Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA

SOURCE: PCT Int. Appl., 980 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 90

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 2001055322	A2	20010802	WO 2001-US1341	20010117
WO 2001055322	A3	20020704		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
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AU 2001041413	A5	20010807	AU 2001-41413	20010117
AU 2001041416	A5	20010807	AU 2001-41416	20010117
AU 2001041417	A5	20010807	AU 2001-41417	20010117
AU 2001050770	A5	20010807	AU 2001-50770	20010117
AU 2001055162	A5	20010807	AU 2001-55162	20010117
US 2002042096	A1	20020411	US 2001-764887	20010117
US 2002077270	A1	20020620	US 2001-764848	20010117
US 2002086811	A1	20020704	US 2001-764861	20010117
US 2002086820	A1	20020704	US 2001-764862	20010117
US 2002086821	A1	20020704	US 2001-764881	20010117
US 2002086822	A1	20020704	US 2001-764886	20010117
US 2002086823	A1	20020704	US 2001-764889	20010117
US 2002086330	A1	20020704	US 2001-764893	20010117

Searcher : Shears 308-4994

09/750609

US 2002090615	A1	20020711	US 2001-764878	20010117
US 2002090674	A1	20020711	US 2001-764903	20010117
US 2002094953	A1	20020718	US 2001-764860	20010117
US 2002102638	A1	20020801	US 2001-764846	20010117
US 2002119919	A1	20020829	US 2001-764855	20010117
US 2002132767	A1	20020919	US 2001-764847	20010117
US 2002147140	A1	20021010	US 2001-764877	20010117
US 2002151479	A1	20021017	US 2001-764873	20010117
US 2002161208	A1	20021031	US 2001-764884	20010117
EP 1254147	A2	20021106	EP 2001-928288	20010117
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2002164685	A1	20021107	US 2001-764857	20010117
US 2002173454	A1	20021121	US 2001-764904	20010117
AU 2001052878	A5	20010807	AU 2001-52878	20010129
AU 2001043137	A5	20010814	AU 2001-43137	20010205
US 2002045230	A1	20020418	US 2001-908711	20010720

PRIORITY APPLN. INFO.:

US 2000-179065P	P	20000131
US 2000-180628P	P	20000204
US 2000-184664P	P	20000224
US 2000-186350P	P	20000302
US 2000-189874P	P	20000316
US 2000-190076P	P	20000317
US 2000-198123P	P	20000418
US 2000-205515P	P	20000519
US 2000-209467P	P	20000607
US 2000-214886P	P	20000628
US 2000-215135P	P	20000630
US 2000-216647P	P	20000707
US 2000-216880P	P	20000707
US 2000-217487P	P	20000711
US 2000-217496P	P	20000711
US 2000-218290P	P	20000714
US 2000-220963P	P	20000726
US 2000-220964P	P	20000726
US 2000-224518P	P	20000814
US 2000-224519P	P	20000814
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US 2000-225447P	P	20000814
US 2000-225757P	P	20000814
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US 2000-225759P	P	20000814
US 2000-226279P	P	20000818
US 2000-226681P	P	20000822
US 2000-226868P	P	20000822
US 2000-227182P	P	20000822
US 2000-227009P	P	20000823
US 2000-228924P	P	20000830
US 2000-229343P	P	20000901
US 2000-229344P	P	20000901
US 2000-229287P	P	20000901
US 2000-229345P	P	20000901
US 2000-229509P	P	20000905

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US 2000-229513P	P	20000905
US 2000-231413P	P	20000908
US 2000-232398P	P	20000914
US 2000-234223P	P	20000921
US 2000-234274P	P	20000921
US 2000-234997P	P	20000925
US 2000-235834P	P	20000927
US 2000-236327P	P	20000929
US 2000-236367P	P	20000929
US 2000-236368P	P	20000929
US 2000-236369P	P	20000929
US 2000-236370P	P	20000929
US 2000-236802P	P	20001002
US 2000-237037P	P	20001002
US 2000-237039P	P	20001002
US 2000-237040P	P	20001002
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US 2000-241809P	P	20001020
US 2000-244617P	P	20001101
US 2000-246478P	P	20001108
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US 2000-246524P	P	20001108
US 2000-246609P	P	20001108
US 2000-246613P	P	20001108
US 2000-249207P	P	20001117
US 2000-249208P	P	20001117
US 2000-249210P	P	20001117
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US 2000-249215P	P	20001117
US 2000-249216P	P	20001117
US 2000-249217P	P	20001117
US 2000-249218P	P	20001117
US 2000-249244P	P	20001117
US 2000-249245P	P	20001117
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US 2000-249300P	P	20001117
US 2000-250160P	P	20001201
US 2000-251856P	P	20001208
US 2000-251868P	P	20001208
US 2000-251869P	P	20001208
US 2000-251990P	P	20001208
US 2001-764853	A2	20010117
US 2001-764856	A2	20010117
US 2001-764864	A2	20010117
US 2001-764867	A2	20010117
US 2001-764868	A2	20010117
US 2001-764869	A2	20010117
US 2001-764870	A2	20010117
US 2001-764874	A2	20010117
US 2001-764882	A2	20010117
US 2001-764888	A2	20010117
US 2001-764891	A2	20010117
US 2001-764892	A2	20010117
US 2001-764896	A2	20010117
US 2001-764898	A2	20010117

Searcher : Shears 308-4994

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US 2001-764902 A2 20010117
US 2001-764905 A2 20010117
WO 2001-US1239 A2 20010117
WO 2001-US1307 A2 20010117
WO 2001-US1312 A2 20010117
WO 2001-US1320 A2 20010117
WO 2001-US1329 A2 20010117
WO 2001-US1334 A2 20010117
WO 2001-US1336 A2 20010117
WO 2001-US1339 A2 20010117
WO 2001-US1340 A2 20010117
WO 2001-US1341 W 20010117
WO 2001-US1344 A2 20010117
WO 2001-US1345 A2 20010117
WO 2001-US1347 A2 20010117
WO 2001-US1348 A2 20010117
WO 2001-US1360 A2 20010117

AB The present invention relates to novel proteins. More specifically, 461 isolated nucleic acid mols. are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting or enhancing the prodn. and function of the polypeptides of the present invention.

IT 353342-86-6

RL: PRP (Properties)

(unclaimed nucleotide sequence; human nucleic acids and their encoded proteins and antibodies)

L2 ANSWER 12 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:565197 HCAPLUS

DOCUMENT NUMBER: 135:163396

TITLE: Human nucleic acids and their encoded proteins and antibodies

INVENTOR(S): Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA

SOURCE: PCT Int. Appl., 837 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 90

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001055318	A2	20010802	WO 2001-US1332	20010117
WO 2001055318	A3	20020704		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,				

Searcher : Shears 308-4994

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LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
TG

AU 2001041412	A5	20010807	AU 2001-41412	20010117
AU 2001041414	A5	20010807	AU 2001-41414	20010117
AU 2001047190	A5	20010807	AU 2001-47190	20010117
AU 2001049053	A5	20010807	AU 2001-49053	20010117
AU 2001049054	A5	20010807	AU 2001-49054	20010117
AU 2001050767	A5	20010807	AU 2001-50767	20010117
AU 2001050769	A5	20010807	AU 2001-50769	20010117
AU 2001050770	A5	20010807	AU 2001-50770	20010117
US 2002042096	A1	20020411	US 2001-764887	20010117
US 2002077270	A1	20020620	US 2001-764848	20010117
US 2002086811	A1	20020704	US 2001-764861	20010117
US 2002086820	A1	20020704	US 2001-764862	20010117
US 2002086821	A1	20020704	US 2001-764881	20010117
US 2002086822	A1	20020704	US 2001-764886	20010117
US 2002086823	A1	20020704	US 2001-764889	20010117
US 2002086330	A1	20020704	US 2001-764893	20010117
US 2002090615	A1	20020711	US 2001-764878	20010117
US 2002090674	A1	20020711	US 2001-764903	20010117
US 2002094953	A1	20020718	US 2001-764860	20010117
US 2002102638	A1	20020801	US 2001-764846	20010117
US 2002119919	A1	20020829	US 2001-764855	20010117
US 2002132767	A1	20020919	US 2001-764847	20010117
US 2002147140	A1	20021010	US 2001-764877	20010117
US 2002151479	A1	20021017	US 2001-764873	20010117
US 2002161208	A1	20021031	US 2001-764884	20010117
US 2002164685	A1	20021107	US 2001-764857	20010117
US 2002173454	A1	20021121	US 2001-764904	20010117
EP 1259526	A2	20021127	EP 2001-922230	20010117

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

AU 2001050771 A5 20010820 AU 2001-50771 20010206
PRIORITY APPLN. INFO.:

US 2000-179065P	P	20000131
US 2000-180628P	P	20000204
US 2000-184664P	P	20000224
US 2000-186350P	P	20000302
US 2000-189874P	P	20000316
US 2000-190076P	P	20000317
US 2000-198123P	P	20000418
US 2000-205515P	P	20000519
US 2000-209467P	P	20000607
US 2000-214886P	P	20000628
US 2000-215135P	P	20000630
US 2000-216647P	P	20000707
US 2000-216880P	P	20000707
US 2000-217487P	P	20000711
US 2000-217496P	P	20000711
US 2000-218290P	P	20000714
US 2000-220963P	P	20000726
US 2000-220964P	P	20000726
US 2000-224518P	P	20000814

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US 2000-224519P	P	20000814
US 2000-225213P	P	20000814
US 2000-225214P	P	20000814
US 2000-225266P	P	20000814
US 2000-225267P	P	20000814
US 2000-225268P	P	20000814
US 2000-225270P	P	20000814
US 2000-225447P	P	20000814
US 2000-225757P	P	20000814
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US 2000-226279P	P	20000818
US 2000-226681P	P	20000822
US 2000-226868P	P	20000822
US 2000-227182P	P	20000822
US 2000-227009P	P	20000823
US 2000-228924P	P	20000830
US 2000-229343P	P	20000901
US 2000-229345P	P	20000901
US 2000-229287P	P	20000901
US 2000-229344P	P	20000901
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US 2000-229513P	P	20000905
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US 2000-236802P	P	20001002
US 2000-237037P	P	20001002
US 2000-237039P	P	20001002
US 2000-237040P	P	20001002
US 2000-241785P	P	20001020
US 2000-241809P	P	20001020
US 2000-244617P	P	20001101
US 2000-246478P	P	20001108
US 2000-246523P	P	20001108
US 2000-246524P	P	20001108
US 2000-246609P	P	20001108
US 2000-246613P	P	20001108
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US 2000-249212P	P	20001117
US 2000-249213P	P	20001117
US 2000-249214P	P	20001117
US 2000-249215P	P	20001117
US 2000-249216P	P	20001117
US 2000-249217P	P	20001117
US 2000-249218P	P	20001117
US 2000-249244P	P	20001117

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US 2000-249245P P 20001117
US 2000-249264P P 20001117
US 2000-249265P P 20001117
US 2000-249297P P 20001117
US 2000-249299P P 20001117
US 2000-249300P P 20001117
US 2000-250160P P 20001201
US 2000-250391P P 20001201
US 2000-251030P P 20001205
US 2000-251988P P 20001205
US 2000-256719P P 20001205
US 2000-251856P P 20001208
US 2000-251868P P 20001208
US 2000-251869P P 20001208
WO 2001-US1332 W 20010117

AB The present invention relates to novel nervous system-related polynucleotides and the polypeptides encoded thereby, and to the use of such for detecting and/or treating disorders of the nervous system. More specifically, 598 isolated nervous system-assocd. cDNA mols. are provided encoding novel polypeptides. Novel nervous system-related polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human nervous system-assocd. polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the nervous system. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the prodn. and function of the polypeptides of the present invention.

IT **352813-12-8P**

RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)

(nucleotide sequence; human nervous system-specific nucleic acids and their encoded proteins and antibodies)

L2 ANSWER 13 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:564770 HCAPLUS

DOCUMENT NUMBER: 135:163373

TITLE: Protein and cDNA sequences of potential novel human transport proteins

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA

SOURCE: PCT Int. Appl., 811 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 90

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001054472	A2	20010802	WO 2001-US1307	20010117
WO 2001054472	A3	20020131		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH,

Searcher : Shears 308-4994

09/750609

GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, NE, SN, TD, TG

AU 2001062899	A5	20011018	AU 2001-62899	20010117
US 2002042096	A1	20020411	US 2001-764887	20010117
US 2002077270	A1	20020620	US 2001-764848	20010117
US 2002086811	A1	20020704	US 2001-764861	20010117
US 2002086820	A1	20020704	US 2001-764862	20010117
US 2002086821	A1	20020704	US 2001-764881	20010117
US 2002086822	A1	20020704	US 2001-764886	20010117
US 2002086823	A1	20020704	US 2001-764889	20010117
US 2002086330	A1	20020704	US 2001-764893	20010117
US 2002090615	A1	20020711	US 2001-764878	20010117
US 2002090674	A1	20020711	US 2001-764903	20010117
US 2002094953	A1	20020718	US 2001-764860	20010117
US 2002102638	A1	20020801	US 2001-764846	20010117
US 2002119919	A1	20020829	US 2001-764855	20010117
US 2002132767	A1	20020919	US 2001-764847	20010117
US 2002147140	A1	20021010	US 2001-764877	20010117
US 2002151479	A1	20021017	US 2001-764873	20010117
US 2002161208	A1	20021031	US 2001-764884	20010117
EP 1254272	A2	20021106	EP 2001-937134	20010117

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

US 2002164685	A1	20021107	US 2001-764857	20010117
US 2002173454	A1	20021121	US 2001-764904	20010117
US 2002045230	A1	20020418	US 2001-908711	20010720

PRIORITY APPLN. INFO.:

US 2000-179065P	P	20000131
US 2000-180628P	P	20000204
US 2000-184664P	P	20000224
US 2000-186350P	P	20000302
US 2000-189874P	P	20000316
US 2000-190076P	P	20000317
US 2000-198123P	P	20000418
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US 2000-217487P	P	20000711
US 2000-217496P	P	20000711
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US 2000-220963P	P	20000726
US 2000-220964P	P	20000726
US 2000-225270P	P	20000814
US 2000-225757P	P	20000814
US 2000-224518P	P	20000814
US 2000-224519P	P	20000814
US 2000-225267P	P	20000814
US 2000-225268P	P	20000814
US 2000-225447P	P	20000814
US 2000-225758P	P	20000814
US 2000-226868P	P	20000822

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US 2000-228924P	P	20000830
US 2000-229287P	P	20000901
US 2000-229343P	P	20000901
US 2000-229344P	P	20000901
US 2000-229345P	P	20000901
US 2000-229509P	P	20000905
US 2000-229513P	P	20000905
US 2000-231413P	P	20000908
US 2000-232398P	P	20000914
US 2000-234223P	P	20000921
US 2000-234274P	P	20000921
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US 2000-236370P	P	20000929
US 2000-236802P	P	20001002
US 2000-237037P	P	20001002
US 2000-237039P	P	20001002
US 2000-237040P	P	20001002
US 2000-241785P	P	20001020
US 2000-241809P	P	20001020
US 2000-244617P	P	20001101
US 2000-246478P	P	20001108
US 2000-246523P	P	20001108
US 2000-246524P	P	20001108
US 2000-246609P	P	20001108
US 2000-246613P	P	20001108
US 2000-249207P	P	20001117
US 2000-249208P	P	20001117
US 2000-249210P	P	20001117
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US 2000-249212P	P	20001117
US 2000-249213P	P	20001117
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US 2000-249217P	P	20001117
US 2000-249218P	P	20001117
US 2000-249244P	P	20001117
US 2000-249245P	P	20001117
US 2000-249297P	P	20001117
US 2000-249299P	P	20001117
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US 2000-250160P	P	20001201
US 2000-251856P	P	20001208
US 2000-251868P	P	20001208
US 2000-251869P	P	20001208
US 2000-251990P	P	20001208
US 2001-764853	A2	20010117
US 2001-764856	A2	20010117
US 2001-764864	A2	20010117
US 2001-764867	A2	20010117
US 2001-764868	A2	20010117
US 2001-764869	A2	20010117
US 2001-764870	A2	20010117
US 2001-764874	A2	20010117

Searcher : Shears 308-4994

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US 2001-764882 A2 20010117
US 2001-764888 A2 20010117
US 2001-764891 A2 20010117
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US 2001-764898 A2 20010117
US 2001-764902 A2 20010117
US 2001-764905 A2 20010117
WO 2001-US1239 A2 20010117
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WO 2001-US1312 A2 20010117
WO 2001-US1320 A2 20010117
WO 2001-US1329 A2 20010117
WO 2001-US1334 A2 20010117
WO 2001-US1336 A2 20010117
WO 2001-US1339 A2 20010117
WO 2001-US1340 A2 20010117
WO 2001-US1341 A2 20010117
WO 2001-US1344 A2 20010117
WO 2001-US1345 A2 20010117
WO 2001-US1347 A2 20010117
WO 2001-US1348 A2 20010117
WO 2001-US1360 A2 20010117

AB The present invention relates to novel polynucleotides and the polypeptides encoded by these polynucleotides, and the use of such proteins, which are potential transport proteins, for diagnosing, treating, preventing disorders related to these novel peptides. More specifically, 284 isolated cDNA mols. are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing novel human polynucleotides and/or polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the prodn. and function of the polypeptides of the present invention.

IT 353546-78-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; protein and cDNA sequences of potential novel human transport proteins)

L2 ANSWER 14 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:563397 HCAPLUS

DOCUMENT NUMBER: 135:315743

TITLE: Evidence for the presence of two novel pestivirus species

AUTHOR(S): Avalos-Ramirez, Ramiro; Orlich, Michaela; Thiel, Heinz-Jurgen; Becher, Paul

CORPORATE SOURCE: Institut fur Virologie (FB Veterinarmedizin), Justus-Liebig-Universitat, Giessen, D-35392, Germany

SOURCE: Virology (2001), 286(2), 456-465

CODEN: VIRLAX; ISSN: 0042-6822

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

Searcher : Shears 308-4994

AB The genus Pestivirus of the family Flaviviridae comprises 4 species, namely Bovine viral diarrhea virus-1 (BVDV-1), BVDV-2, Border disease virus (BDV), and Classical swine fever virus (CSFV). Comparative analyses of partial sequences have suggested that pestivirus isolates from giraffe (Giraffe-1) and reindeer (Reindeer-1) are distinct from the established species. This study reports the complete genomic sequences of pestivirus strains Giraffe-1 and Reindeer-1. Comparative sequence analyses revealed considerable differences among Giraffe-1, Reindeer-1, and the currently recognized pestivirus species. Phylogenetic anal. of the complete coding sequences of these 2 strains, along with 13 other sequences representing the 4 established species, indicated that CSFV, BDV, and Reindeer-1 have bifurcated from one common branch and BVDV-1 and BVDV-2 from another. In the former branch, BDV and the pestivirus from reindeer are more similar to each other than to CSFV. The giraffe pestivirus is equally distinct from both major branches. In addn., the antigenic relatedness of pestivirus isolates covering the obsd. major genetic groups was studied by cross-neutralization assays. A clustering procedure on the basis of antigenic differences indicated the presence of 6 major groups corresponding to the genetically defined groups. Taken together, the results of these analyses addressing both nucleotide sequence relatedness and serol. relatedness argue for the inclusion of Giraffe-1 and Reindeer-1 as the 1st members of 2 sep. novel species within the genus Pestivirus. (c) 2001 Academic Press.

IT 244376-77-0, RNA (pestivirus isolate Giraffe-1)

RL: PRP (Properties)

(nucleotide sequence; evidence for the presence of two novel pestivirus species)

REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 15 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:526219 HCAPLUS

DOCUMENT NUMBER: 135:117965

TITLE: Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders

INVENTOR(S): Chu, Tom; Blumenfeld, Marta; Cohen, Daniel

PATENT ASSIGNEE(S): Genset, Fr.

SOURCE: PCT Int. Appl., 519 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001051659	A2	20010719	WO 2001-IB116	20010111
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			

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RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
TG

PRIORITY APPLN. INFO.:

US 2000-175854P P 20000113

AB The invention provides 271 polynucleotides including biallelic markers derived from genes involved in central nervous system (CNS) disorders and from genomic regions flanking those genes. Microsequencing and amplification primers hybridizing to regions flanking these biallelic markers, and hybridization probes for their detection, are also provided. This invention also provides polynucleotides and methods suitable for genotyping a nucleic acid contg. sample for one or more biallelic markers of the invention. Further, the invention provides methods to detect a statistical correlation between a biallelic marker allele and a phenotype and/or between a biallelic marker haplotype and a phenotype.

IT 350526-60-2 350526-65-7 350530-97-1

RL: ADV (Adverse effect, including toxicity); ANT (Analyte); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders)

L2 ANSWER 16 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:489671 HCAPLUS

DOCUMENT NUMBER: 135:88017

TITLE: Genetic mutation in human norepinephrine transporter gene exon 9 underlying orthostatic intolerance

INVENTOR(S): Robertson, David; Blakely, Randy D.

PATENT ASSIGNEE(S): Vanderbilt University, USA

SOURCE: PCT Int. Appl., 134 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001048246	A1	20010705	WO 2000-US35491	20001228
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.:

US 1999-173682P P 19991229

US 2000-175456P P 20000111

AB Isolated polynucleotide mols. and peptides of encoded human norepinephrine (NE) transporter are used in the anal. of human NE transporter variants. By analyzing genomic DNA or amplified genomic

DNA, or amplified cDNA derived from mRNA, it is possible to type a human NE transporter with regard to the human NE transporter polymorphism. Two mutations, c154a and g237c, were identified in exon 9 of human NE gene. The g237c mutation results in a coding alteration of alanine to proline (A457P) within a highly conserved region of transmembrane domain 9. The invention relates to diagnosing and treating NE transport impairment, and disorders assocd. with NE transport impairment, such as orthostatic intolerance.

IT 136252-69-2, DNA (human norepinephrine-transporting protein cDNA) 349512-93-2 349513-00-4 349513-02-6

RL: ADV (Adverse effect, including toxicity); ANT (Analyte); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; genetic mutation in human norepinephrine transporter gene exon 9 underlying orthostatic intolerance)

IT 349512-96-5

RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe RB704 for mutant allele A457P of NE transporter gene; genetic mutation in human norepinephrine transporter gene exon 9 underlying orthostatic intolerance)

IT 349512-95-4

RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe RB704 for wild type allele A457 of NE transporter gene; genetic mutation in human norepinephrine transporter gene exon 9 underlying orthostatic intolerance)

IT 171871-58-2 349515-47-5

RL: PRP (Properties)
(unclaimed nucleotide sequence; genetic mutation in human norepinephrine transporter gene exon 9 underlying orthostatic intolerance)

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 17 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:338761 HCAPLUS

DOCUMENT NUMBER: 134:349020

TITLE: Tissue-specific genes of diagnostic import

INVENTOR(S): Sornasse, Thierry; Seilhamer, Jeffrey J.; Watson, George A.

PATENT ASSIGNEE(S): Incyte Genomics, Inc., USA

SOURCE: PCT Int. Appl., 328 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001032927	A2	20010510	WO 2000-US30396	20001102
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,				

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LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
TG

EP 1255859 A2 20021113 EP 2000-976921 20001102

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRIORITY APPLN. INFO.:

US 1999-163508P P 19991104

WO 2000-US30396 W 20001102

AB The present invention relates to a compn. comprising a plurality of polynucleotides which are cell- and/or tissue-specific and which may be used in their entirety or in part as refs. in producing an expression profile that defines a metabolic or developmental process, treatment, condition, disease, or disorder. Thus, 208 cDNA fragments (and extended sequences) are provided which are specifically expressed in human heart muscle, uterus, ovary, stomach, intestine, lung, liver, kidney, pancreas, and brain tissues. This ref. set may be used in its entirety or in part in arrays to produce expression profiles.

IT 339138-73-7

RL: ARU (Analytical role, unclassified); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; tissue-specific genes of diagnostic import)

L2 ANSWER 18 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:326896 HCAPLUS

DOCUMENT NUMBER: 134:336596

TITLE: Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library

AUTHOR(S): Konno, Hideaki; Fukunishi, Yoshifumi; Shibata, Kazuhiro; Itoh, Masayoshi; Carninci, Piero; Sugahara, Yuichi; Hayashizaki, Yoshihide

CORPORATE SOURCE: Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center, Yokohama, 230-0045, Japan

SOURCE: Genome Research (2001), 11(2), 281-289

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Computer-based methods for constructing a nonredundant mouse full-length cDNA library were developed. The cDNA library construction process comprises assessment of library quality, sequencing the 3' ends of inserts and clustering, and completing a re-array to generate a nonredundant library from a redundant one. After the cDNA libraries are generated, the 5' ends of the inserts were sequenced to check the quality of the library; then the sequencing priority of each library was detd. Selected libraries undergo large-scale sequencing of the 3' ends of the inserts and clustering of the tag sequences. After clustering, the nonredundant library is constructed from the original libraries, which have

redundant clones. All libraries, plates, clones, sequences, and clusters are uniquely identified, and all information is saved in the database according to this identifier. At press time, the system has been in place for the past two years; 939,725 3' end sequences have been clustered into 127,385 groups from 227 cDNA libraries/sublibraries. The sequence data is available in GenBank with the Accession Nos. AV000001-AV175734, AV204013-AV382295, and BB561685-BB609425. [This abstr. record is the sixty-third of 82 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **248623-29-2**, GenBank AV335397

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; computer-based methods for the mouse full-length cDNA encyclopedia and real-time sequence clustering for construction of a nonredundant cDNA library)

L2 ANSWER 19 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:505220 HCAPLUS

DOCUMENT NUMBER: 133:100246

TITLE: Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, *Porphyra yezoensis*

AUTHOR(S): Nikaido, Itoshi; Asamizu, Erika; Nakajima, Maiko; Nakamura, Yasukazu; Saga, Naotsune; Tabata, Satoshi

CORPORATE SOURCE: Graduate School of Marine Science and Technology, Tokai University, Shizuoka, 424-8610, Japan

SOURCE: DNA Research (2000), 7(3), 223-227
CODEN: DARSE8; ISSN: 1340-2838

PUBLISHER: Universal Academy Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A total of 10,154 5'-end expressed sequence tags (EST) were established from the normalized and size-selected cDNA libraries of a marine red alga, *Porphyra yezoensis*. Among the ESTs, 2140 were unique species, and the remaining 8014 were grouped into 1127 species. Database search of the 3267 non-redundant ESTs by BLAST algorithm showed that the sequences of 1080 species (33.1%) have similarity to those of registered genes from various organisms including higher plants, mammals, yeasts, and cyanobacteria, while 2187 (66.9%) are novel. Codon usage anal. in the coding regions of 101 non-redundant EST groups showing significant similarity to known genes indicated the higher GC contents at the third position of codons (79.4%) than the first (62.2%) and the second position (45.0%), suggesting that the genome has been exposed to high GC pressure during evolution. The EST sequences appear in the GenBank database with accession nos. AV429311-AV439464. [This abstr. record is the first of 2 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **273822-66-5**

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; expressed sequence tags from a leafy gametophyte of *Porphyra yezoensis*)

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REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 20 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:133722 HCAPLUS

DOCUMENT NUMBER: 132:176644

TITLE: Secreted proteins from human cDNA libraries

INVENTOR(S): Jacobs, Kenneth; McCoy, John M.; Lavallie,
Edward R.; Collins Racie, Lisa A.; Evans,
Cheryl; Merberg, David; Treacy, Maurice;
Agostino, Michael J.; Steininger, Robert J., II;
Spaulding, Vikki; Wong, Gordon G.; Clark, Hilar
F.; Fechtel, Kim

PATENT ASSIGNEE(S): Genetics Institute, Inc., USA

SOURCE: PCT Int. Appl., 641 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000009552	A1	20000224	WO 1999-US18298	19990813
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
CA 2339047	AA	20000224	CA 1999-2339047	19990813
AU 9955570	A1	20000306	AU 1999-55570	19990813
EP 1112286	A1	20010704	EP 1999-942123	19990813
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
JP 2002522062	T2	20020723	JP 2000-565001	19990813
PRIORITY APPLN. INFO.:			US 1998-96622P	P 19980814
			US 1998-96815P	P 19980817
			US 1998-99229P	P 19980904
			US 1998-105368P	P 19981023
			US 1999-115234P	P 19990108
			US 1999-119931P	P 19990212
			US 1999-120575P	P 19990218
			US 1999-132020P	P 19990430
			US 1999-148424P	P 19990811
			WO 1999-US18298	W 19990813

AB Novel polynucleotides and the proteins encode thereby are disclosed. Nucleotide and amino acid sequences are reported for full-length clones isolated using methods which are selective for human cDNAs encoding secreted proteins. Eighty clones were isolated from various human fetal and adult tissue cDNA libraries. Recombinant prodn. of the secreted proteins and their mature forms can be achieved by std. techniques, and the proteins may have biol. activities (no data) useful for therapeutic applications.

IT **259161-10-9DP**, subfragments are claimed
 RL: BPN (Biosynthetic preparation); PRP (Properties); THU
 (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES
 (Uses)

(nucleotide sequence; secreted proteins from human cDNA
 libraries)

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR
 THIS RECORD. ALL CITATIONS AVAILABLE IN
 THE RE FORMAT

L2 ANSWER 21 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:585607 HCAPLUS

DOCUMENT NUMBER: 132:31438

TITLE: Genetic diversity of pestiviruses:
 identification of novel groups and implications
 for classification

AUTHOR(S): Becher, Paul; Orlich, Michaela; Kosmidou,
 Alexandra; Konig, Matthias; Baroth, Martina;
 Thiel, Heinz-Jurgen

CORPORATE SOURCE: Institut fur Virologie (FB Veterinarmedizin),
 Justus-Liebig-Universitat, Giessen, D-35392,
 Germany

SOURCE: Virology (1999), 262(1), 64-71

CODEN: VIRLAX; ISSN: 0042-6822

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The complete Npro coding sequences were detd. for 16 pestiviruses
 isolated from cattle, pig, and several wild ruminant species
 including reindeer, bison, deer, and bongo. Phylogenetic anal.
 enabled the segregation of pestiviruses into the established species
 bovine viral diarrhea virus-1 (BVDV-1), BVDV-2, border disease virus
 (BDV), and classical swine fever virus (CSFV). For BVDV-1 five
 distinct subgroups were identified, while BVDV-2, BDV, and CSFV were
 each subdivided into two subgroups. The virus isolates from bongo
 and deer as well as one porcine virus isolate belong to BVDV-1.
 Interestingly, the isolates from reindeer and bison are distinct
 from the established pestivirus species. The Npro sequences from
 these two viruses are more similar to BDV than to the other
 pestivirus species. Calcn. of the pairwise evolutionary distances
 allowed a clear sepn. of the categories species, subgroup, and
 isolate only when the reindeer/bison viruses were considered as
 members of an addnl. pestivirus species. Furthermore, the entire E2
 coding sequences of a representative set of virus isolates covering
 all recognized species and subgroups were studied. Segregation of
 pestiviruses based on the E2 region was identical with that obtained
 with the Npro sequences. (c) 1999 Academic Press.

IT **244376-77-0**, GenBank AF144617

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)

(nucleotide sequence; genetic diversity of pestiviruses:
 identification of novel groups and implications for
 classification)

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE
 FOR THIS RECORD. ALL CITATIONS AVAILABLE
 IN THE RE FORMAT

L2 ANSWER 22 OF 27 HCAPLUS COPYRIGHT 2002 ACS

09/750609

ACCESSION NUMBER: 1998:745962 HCAPLUS
DOCUMENT NUMBER: 130:21244
TITLE: Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
AUTHOR(S): Nagase, Takahiro; Ishikawa, Ken-ichi; Suyama, Mikita; Kikuno, Reiko; Miyajima, Nobuyuki; Tanaka, Ayako; Kotani, Hirokazu; Nomura, Nobuo; Ohara, Osamu
CORPORATE SOURCE: Kazusa DNA Research Institute, Yana, Kisarazu, Chiba, 292-0812, Japan
SOURCE: DNA Research (1998), 5(5), 277-286
CODEN: DARSE8; ISSN: 1340-2838
PUBLISHER: Kazusa DNA Research Institute
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In a series of projects for accumulating sequence information on the coding sequences of unidentified human genes, the sequences of 100 cDNA clones were detd. from a set of size-fractionated human brain cDNA libraries, and the coding sequences of the corresponding genes, named KIAA0711 to KIAA0810. were predicted. These cDNA clones were selected according to their coding potentials of large proteins (.gtoreq.50 kDa) in vitro. The av. sizes of the inserts and corresponding open reading frames were 4.3 kb and 2.6 kb (869 amino acid residues), resp. Sequence analyses against the public databases indicated that the predicted coding sequences of 78 genes were similar to those of known genes, 64% of which (50 genes) were categorized as proteins functionally related to cell signaling/communication, cell structure/motility and nucleic acid management. As addnl. information concerning genes characterized in this study, the chromosomal locations of the clones were detd. by using human-rodent hybrid panels and the expression profiles among 10 human tissues were examd. by reverse transcription-coupled polymerase chain reaction which was substantially improved by ELISA.
IT 216296-35-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; complete sequences of 100 new cDNA clones from human brain which code for large proteins in vitro)
REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 23 OF 27 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:676582 HCAPLUS
DOCUMENT NUMBER: 125:321016
TITLE: Molecular cloning and organization of the coding region of the human norepinephrine transporter gene. [Erratum to document cited in CA124:48558]
AUTHOR(S): Poerzgen, Peter; Boenisch, Heinz; Bruess, Michael
CORPORATE SOURCE: Inst. Pharmacol. Toxicol., Univ. Bonn, Bonn, D-53113, Germany
SOURCE: Biochemical and Biophysical Research Communications (1996), 227(2), 642-644
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic

Searcher : Shears 308-4994

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The authors incorrectly indicated that exon 4 is located 18 kb downstream of exon 3. Consequently, the intron size for exon 3 should read 12 kb and intron size for exon 4 should read 6.5 instead of 0.7 kb. Fig. 1 and Table 1 are reprinted to correct these errors. The errors were not reflected in the abstr. or the index entries.

IT 171871-58-2

RL: PRP (Properties)

(mol. cloning and organization of coding region of human norepinephrine transporter gene (Erratum))

L2 ANSWER 24 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1995:881263 HCAPLUS

DOCUMENT NUMBER: 124:48558

TITLE: Molecular cloning and organization of the coding region of the human norepinephrine transporter gene

AUTHOR(S): Poerzgen, Peter; Boenisch, Heinz; Bruess, Michael

CORPORATE SOURCE: Inst. Pharmacol. Toxicol., Univ. Bonn, Bonn, D-53113, Germany

SOURCE: Biochemical and Biophysical Research Communications (1995), 215(3), 1145-50
CODEN: BBRCA9; ISSN: 0006-291X

PUBLISHER: Academic

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A .lambda. phage genomic library was screened with the digoxigenin labeled cDNA of the human norepinephrine transporter (hNET). Six overlapping .lambda. clones were analyzed by restriction enzyme anal. and sequencing of the exon-intron boundaries. The coding region of the hNET gene was found to be encoded by 14 exons, spanning 45 kb from the start to the stop codon, disrupted by 13 introns. The organization of the gene is highly homologous to other known neurotransmitter transporter genes. However, the hNET gene differs from the other genes in that it has an addnl. exon encoding the C-terminus of the protein. The gene structure shows two large introns in the 5'-region and a cluster of 11 exons in the 3'-region. All exon-intron junctions contain the gt/ag consensus splice site. Knowledge of the gene structure of the antidepressant-sensitive hNET should facilitate investigation of its potential role in psychiatric disorders.

IT 171871-58-2

RL: PRP (Properties)

(nucleotide sequence of; mol. cloning and organization of coding region of human norepinephrine transporter gene)

L2 ANSWER 25 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1993:575149 HCAPLUS

DOCUMENT NUMBER: 119:175149

TITLE: Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library

AUTHOR(S): Adams, Mark D.; Soares, M. Bento; Kerlavage, Anthony R.; Fields, Chris; Venter, J. Craig

CORPORATE SOURCE: NINDS, Rockville, MD, 20892, USA

09/750609

SOURCE: Nature Genetics (1993), 4(4), 373-80
CODEN: NGENEC; ISSN: 1061-4036

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A human infant brain cDNA library, made specifically for prodn. of expressed sequence tags (ESTs) was evaluated by partial sequencing of >1600 clones. Advantages of this library, constructed for EST sequencing, include the use of directional cloning, size selection, very low nos. of mitochondrial and ribosomal transcripts, short poly(A) tails, few non-recombinants, and a broad representation of transcripts. About 37% of the clones were identified, based on matches to >320 different genes in the public databases. Of these, 2 proteins similar to the Alzheimer's disease amyloid precursor were identified.

IT **149643-85-6**, GenBank T08889
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

L2 ANSWER 26 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1993:95123 HCAPLUS

DOCUMENT NUMBER: 118:95123

TITLE: A cDNA clone encoding a human norepinephrine transporter and its expression in transgenic cells

INVENTOR(S): Amara, Susan G.; Pacholczyk, Tadeusz; Blakely, Randy D.

PATENT ASSIGNEE(S): Oregon Health Sciences University, USA

SOURCE: PCT Int. Appl., 36 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
WO 9217568	A1	19921015	WO 1992-US1376	19920220	
W: AU, CA, DK, FI, JP, NO					
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, MC, NL, SE					
CA 2106190	AA	19920929	CA 1992-2106190	19920220	
AU 9217742	A1	19921102	AU 1992-17742	19920220	
EP 602044	A1	19940622	EP 1992-910856	19920220	
R: AT, BE, CH, DE, DK, FR, GB, IT, LI, LU, NL, SE					
JP 07505040	T2	19950608	JP 1992-509934	19920220	
DK 9301075	A	19930923	DK 1993-1075	19930923	
NO 9303378	A	19930928	NO 1993-3378	19930923	
PRIORITY APPLN. INFO.:				US 1991-676980	19910328
				WO 1992-US1376	19920220

AB The human norepinephrine transporter, its cDNA, and cells expressing the cDNA are claimed. The cDNA from human neuroblastoma cell line SK-N-SH for the receptor was cloned in COS-1 cells by expression. There was a 46% overall similarity between the amino acid sequences of this transporter and that of the rat GABA transporter; no other significant similarities were found. In Northern blotting expts., 2 mRNAs of 3.6 and 5.8 kb were identified. The 5.8 kb mRNA appeared to correspond to the neuronal-specific transporter protein of the invention. The 3.6 kb mRNA may represent a glial-specific form. HeLa cells transfected with the transporter cDNA displayed

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Na-dependent norepinephrine accumulation. Accumulation was blocked by cocaine (KI 140 nM) and D-amphetamine (KI 56 nM), among other drugs.

IT 136252-70-5

RL: PRP (Properties)
(nucleotide sequence of)

IT 136252-69-2, Deoxyribonucleic acid (human
norepinephrine-transporting protein messenger RNA-complementary)

RL: PRP (Properties)
(nucleotide sequence of, complete)

L2 ANSWER 27 OF 27 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1991:552186 HCAPLUS

DOCUMENT NUMBER: 115:152186

TITLE: Expression cloning of a cocaine- and
antidepressant-sensitive human noradrenaline
transporter

AUTHOR(S): Pacholczyk, Tadeusz; Blakely, Randy D.; Amara,
Susan G.

CORPORATE SOURCE: Sch. Med., Yale Univ., New Haven, CT, 06510, USA

SOURCE: Nature (London, United Kingdom) (1991),
350(6316), 350-4

CODEN: NATUAS; ISSN: 0028-0836

DOCUMENT TYPE: Journal

LANGUAGE: English

AB At most synapses, chem. signalling is terminated by a rapid
reaccumulation of neurotransmitter into presynaptic terminals.
Uptake systems for the biogenic amines are the initial site of
action for therapeutic antidepressants and drugs such as cocaine and
the amphetamines. A cDNA clone encoding a human noradrenaline
transporter was isolated. The cDNA sequence predicts a protein of
617 amino acids, with 12-13 highly hydrophobic regions compatible
with membrane-spanning domains. Expression of the cDNA clone in
transfected HeLa cells indicates that noradrenaline transport
activity is sodium-dependent and sensitive to selective
noradrenaline transport inhibitors. Transporter RNA is localized to
the brainstem and the adrenal gland. The predicted protein sequence
demonstrates significant amino-acid identity with the
Na⁺/γ-aminobutyric acid transporter, thus identifying a new
gene family for neurotransmitter transporter proteins.

IT 136252-69-2, Deoxyribonucleic acid (human
norepinephrine-transporting protein messenger RNA-complementary)

136252-70-5
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

E1 THROUGH E30 ASSIGNED

FILE=REGISTRY ENTERED AT 10:22:22 ON 12 DEC 2002

L3 30 SEA FILE=REGISTRY ABB=ON PLU=ON (136252-70-5/BI OR
136252-69-2/BI OR 171871-58-2/BI OR 244376-77-0/BI OR
149643-85-6/BI OR 216296-35-4/BI OR 248623-29-2/BI OR
259161-10-9/BI OR 273822-66-5/BI OR 283872-10-6/BI OR
285540-13-8/BI OR 312980-59-9/BI OR 339138-73-7/BI OR
349512-93-2/BI OR 349512-95-4/BI OR 349512-96-5/BI OR
349513-00-4/BI OR 349513-02-6/BI OR 349515-47-5/BI OR
350526-60-2/BI OR 350526-65-7/BI OR 350530-97-1/BI OR
352813-12-8/BI OR 353342-86-6/BI OR 353546-78-8/BI OR

Searcher : Shears 308-4994

09/750609

365592-77-4/BI OR 368618-05-7/BI OR 376407-32-8/BI OR
391524-07-5/BI OR 438805-25-5/BI)

L3 ANSWER 1 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **438805-25-5** REGISTRY
CN DNA (human clone WO0160860-Table 8 prostate gland tumor-associated
protein cDNA fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 426: PN: WO0160860 TABLE: 8 claimed DNA
SQL 445
MF Unspecified
CI MAN

REFERENCE 1: 137:58620

L3 ANSWER 2 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **391524-07-5** REGISTRY
CN DNA (human gene NAT1 cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank M65105
SQL 1983
MF Unspecified
CI MAN

REFERENCE 1: 137:88421

L3 ANSWER 3 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **376407-32-8** REGISTRY
CN DNA (human clone HCEMU86 protein cDNA plus flanks) (9CI) (CA INDEX
NAME)
OTHER NAMES:
CN 1026: PN: WO0190304 SEQID: 1036 claimed DNA
SQL 2520
MF Unspecified
CI MAN

REFERENCE 1: 136:15957

L3 ANSWER 4 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **368618-05-7** REGISTRY
CN DNA (Pan troglodytes clone PTB-102I22.R genome survey sequence)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AG100084
SQL 859
MF Unspecified
CI MAN

REFERENCE 1: 136:129773

L3 ANSWER 5 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **365592-77-4** REGISTRY
CN DNA (human clone WO0175067-SEQID-1856 protein cDNA plus flanks)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1850: PN: WO0175067 SEQID: 1856 claimed DNA
SQL 549
MF Unspecified

09/750609

CI MAN

REFERENCE 1: 135:299570

L3 ANSWER 6 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **353546-78-8** REGISTRY
CN DNA (human clone HCEMU86 262-amino acid protein cDNA plus 3'-flank)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 223: PN: WO0154472 SEQID: 232 claimed DNA
SQL 2522
MF Unspecified
CI MAN

REFERENCE 1: 135:163373

L3 ANSWER 7 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **353342-86-6** REGISTRY
CN 1703: PN: WO0155322 SEQID: 1704 unclaimed DNA (9CI) (CA INDEX NAME)
SQL 15857
MF Unspecified
CI MAN

REFERENCE 1: 135:163399

L3 ANSWER 8 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **352813-12-8** REGISTRY
CN DNA (human clone HCEMU86 nervous system-associated protein
fragment-specifying cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 308: PN: WO0155318 SEQID: 318 claimed DNA
SQL 2159
MF Unspecified
CI MAN

REFERENCE 1: 135:163396

L3 ANSWER 9 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **350530-97-1** REGISTRY
CN DNA (human gene NET plus flanks 160755-nucleotide fragment) (9CI)
(CA INDEX NAME)
OTHER NAMES:
CN 544: PN: WO0151659 SEQID: 544 claimed DNA
SQL 160755
MF Unspecified
CI MAN

REFERENCE 1: 135:117965

L3 ANSWER 10 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **350526-65-7** REGISTRY
CN DNA (human gene NET biallelic marker 16-2-187-containing fragment)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 104: PN: WO0151659 SEQID: 104 claimed DNA
SQL 920
MF Unspecified
CI MAN

09/750609

REFERENCE 1: 135:117965

L3 ANSWER 11 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **350526-60-2** REGISTRY
CN DNA (human gene NET biallelic marker 16-2-76-containing fragment)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 99: PN: WO0151659 SEQID: 99 claimed DNA
SQL 920
MF Unspecified
CI MAN

REFERENCE 1: 135:117965

L3 ANSWER 12 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **349515-47-5** REGISTRY
CN DNA, d(C-C-T-T-C-A-G-T-A-C-T-T-T-C-C-T-T-C-C-C-C-C-T-G-T-T-C-T-G-
C-A-T-A-A-C-C-A-A-G) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 5: PN: WO0148246 SEQID: 5 unclaimed DNA
SQL 41
MF Unspecified
CI MAN

REFERENCE 1: 135:88017

L3 ANSWER 13 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **349513-02-6** REGISTRY
CN DNA (human norepinephrine-transporting protein [2-isoleucine,457-
proline] cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 13: PN: WO0148246 SEQID: 13 claimed DNA
SQL 1854
MF Unspecified
CI MAN

REFERENCE 1: 135:88017

L3 ANSWER 14 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **349513-00-4** REGISTRY
CN DNA (human norepinephrine-transporting protein [2-isoleucine] cDNA)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 11: PN: WO0148246 SEQID: 11 claimed DNA
SQL 1854
MF Unspecified
CI MAN

REFERENCE 1: 135:88017

L3 ANSWER 15 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **349512-96-5** REGISTRY
CN DNA, d(C-C-T-T-C-T-C-C-C-C-C-T-G-T-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 10: PN: WO0148246 SEQID: 10 claimed DNA
SQL 15
MF Unspecified

Searcher : Shears 308-4994

09/750609

CI MAN

REFERENCE 1: 135:88017

L3 ANSWER 16 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **349512-95-4** REGISTRY
CN DNA, d(C-C-T-T-C-T-C-G-C-C-C-T-G-T-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 9: PN: WO0148246 SEQID: 9 claimed DNA
SQL 15
MF Unspecified
CI MAN

REFERENCE 1: 135:88017

L3 ANSWER 17 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **349512-93-2** REGISTRY
CN DNA (human norepinephrine-transporting protein [457-proline] cDNA)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3: PN: WO0148246 SEQID: 3 claimed DNA
SQL 1854
MF Unspecified
CI MAN

REFERENCE 1: 135:88017

L3 ANSWER 18 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **339138-73-7** REGISTRY
CN DNA (human brain-specific Incyte clone 1349484.con cDNA fragment)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 396: PN: WO0132927 SEQID: 396 claimed DNA
SQL 4366
MF Unspecified
CI MAN

REFERENCE 1: 134:349020

L3 ANSWER 19 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **312980-59-9** REGISTRY
CN DNA (Mus musculus strain C57BL6/J clone RP23-31401 chromosome 5
fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AC087420
SQL 232869
MF Unspecified
CI MAN

REFERENCE 1: 137:1254

L3 ANSWER 20 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **285540-13-8** REGISTRY
CN DNA (Leishmania major strain Friedlin clone Chr.12) (9CI) (CA INDEX
NAME)
OTHER NAMES:
CN 1667: PN: WO02070737 FIGURE: 6 unclaimed DNA
CN GenBank AL390114

09/750609

SQL 757191
MF Unspecified
CI MAN

REFERENCE 1: 137:246071

L3 ANSWER 21 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **283872-10-6** REGISTRY
CN DNA (mouse strain C57BL/6J clone RPCI-23-442E20 genome survey
sequence) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AZ284882
SQL 181
MF Unspecified
CI MAN

REFERENCE 1: 136:49172

L3 ANSWER 22 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **273822-66-5** REGISTRY
CN DNA (Porphyra yezoensis strain TU-1 clone PM037d06-r EST (expressed
sequence tag)) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AV434035
SQL 543
MF Unspecified
CI MAN

REFERENCE 1: 133:100246

L3 ANSWER 23 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **259161-10-9** REGISTRY
CN DNA (human clone as180_1 secretory protein cDNA plus flanks) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 157: PN: WO0009552 SEQID: 159 claimed DNA
SQL 3580
MF Unspecified
CI MAN

REFERENCE 1: 132:176644

L3 ANSWER 24 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **248623-29-2** REGISTRY
CN DNA (mouse strain C57BL/6J clone 6330571M18 EST (expressed sequence
tag)) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AV335397
SQL 226
MF Unspecified
CI MAN

REFERENCE 1: 134:336596

L3 ANSWER 25 OF 30 REGISTRY COPYRIGHT 2002 ACS
RN **244376-77-0** REGISTRY
CN RNA (pestivirus strain Giraffe-1 gene E2 fragment) (9CI) (CA INDEX
NAME)

09/750609

OTHER NAMES:

CN GenBank AF144617
SQL 12602
MF Unspecified
CI MAN

REFERENCE 1: 135:315743

REFERENCE 2: 132:31438

L3 ANSWER 26 OF 30 REGISTRY COPYRIGHT 2002 ACS

RN **216296-35-4** REGISTRY

CN DNA (human gene KIAA0736 protein cDNA plus flanks) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AB018279
SQL 4353
MF Unspecified
CI MAN

REFERENCE 1: 130:21244

L3 ANSWER 27 OF 30 REGISTRY COPYRIGHT 2002 ACS

RN **171871-58-2** REGISTRY

CN DNA (human gene NET exon 9 plus exon 10 plus flanks) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human gene NET exon 9 plus exon 10 plus 5'- and 3'-flanking region fragment)

OTHER NAMES:

CN 14: PN: WO0148246 SEQID: 15 unclaimed DNA
SQL 980
MF Unspecified
CI MAN

REFERENCE 1: 135:88017

REFERENCE 2: 125:321016

REFERENCE 3: 124:48558

L3 ANSWER 28 OF 30 REGISTRY COPYRIGHT 2002 ACS

RN **149643-85-6** REGISTRY

CN DNA (human clone HIBBL71 EST (expressed sequence tag) EST06781) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human clone HIBBL71 expressed sequence tag EST06781)

OTHER NAMES:

CN GenBank T08889
SQL 393
MF Unspecified
CI MAN

REFERENCE 1: 119:175149

L3 ANSWER 29 OF 30 REGISTRY COPYRIGHT 2002 ACS

RN **136252-70-5** REGISTRY

09/750609

CN DNA, (human norepinephrine-transporting protein cDNA plus flanks)
(9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid, (human norepinephrine-transporting protein
messenger RNA-complementary plus 5'- and 3'-flanking region
fragment)

OTHER NAMES:

CN DNA (human gene NAT1 noradrenaline transporter cDNA plus flanks)

SQL 1983

MF Unspecified

CI MAN

REFERENCE 1: 135:193985

REFERENCE 2: 135:190398

REFERENCE 3: 118:95123

REFERENCE 4: 115:152186

L3 ANSWER 30 OF 30 REGISTRY COPYRIGHT 2002 ACS

RN 136252-69-2 REGISTRY

CN DNA (human norepinephrine-transporting protein cDNA) (9CI) (CA
INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human norepinephrine-transporting protein
messenger RNA-complementary)

OTHER NAMES:

1: PN: WO0148246 SEQID: 1 claimed DNA

CN DNA (human norepinephrine-transporting protein cDNA)

SQL 1854

MF Unspecified

CI MAN

REFERENCE 1: 135:88017

REFERENCE 2: 118:95123

REFERENCE 3: 115:152186

FILE 'HOME' ENTERED AT 10:22:52 ON 12 DEC 2002